GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on : January 16, 2003, 15:20.22 , Search time 63.8803 Seconds
(without alignments)
14944.909 Million cell updates/sec

Title: US-09-026-459A-36
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Scoring table: IDENTITY_NUC
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Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	3105.4	99.8	3232	1	US-08-038-760-2	Sequence 2, Appli
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c 4	3105.4	99.8	3232	2	US-08-470-091-2	Sequence 2, Appl
5	2415	77.6	2994	1	US-08-204-329-2	Sequence 2, Appli
c 6	2415	77.6	2994	1	US-08-482-627-4	Sequence 4, Appli
7	2415	77.6	2994	3	US-08-801-092-3	Sequence 3, Appli
c 8	2415	77.6	2994	2	US-08-801-092-2	Sequence 2, Appli
9	2413.4	77.5	2994	5	PCT-US94-10357-1	Sequence 5, Appli
10	2412	77.5	2995	2	US-08-959-638-7	Sequence 7, Appli
11	2410.4	77.4	2995	2	US-08-328-673A-7	Sequence 7, Appli
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c 18	59	1.9	7218	2	US-08-232-463-14	Sequence 14, Appli
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23	44	1.4	19124	2	US-08-487-826B-13	Sequence 13, Appl
c 24	43.8	1.4	1056	2	US-09-134-001C-1550	Sequence 1550, Appl
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RESULT 1
US-08-038-760-1
Sequence 1, Application US/08038760
Patent No. 5496731

GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
APPLICANT: Hu, Shi-Xue
APPLICANT: Benedict, William F.
TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/038,760
FILING DATE: 19930325
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7409-025-999

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/9864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3232 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 19..2469

ALIGNMENTS

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Best Local Similarity 100.0%; Pred. No. 0;
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```

TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Pennie & Edmonds
  STREET: 1155 Avenue of the Americas
  CITY: New York
  STATE: New York
  COUNTRY: U.S.A.
  ZIP: 10036-2711
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/026,760
  FILING DATE: 19930325
  CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
  NAME: Poissant, Brian M
  REGISTRATION NUMBER: 28,462
  REFERENCE/DOCKET NUMBER: 7409-025-999
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (212) 790-9090
  TELEFAX: (212) 869-9741/8864
  TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 3232 base pairs
    TYPE: NUCLEIC ACID
    STRANDEDNESS: double
    TOPOLOGY: not relevant
  MOLECULE TYPE: DNA
US-09-026-760-2

Query Match   99.8%; Score 3105.4; DB 1; Length 3232;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3106, Conservative 0, Mismatches 1, Indels 0; Gaps 0;

RESULT 2
US-08-038-760-2/c
Sequence 2, Application US/08038760
Patent No. 5496731
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
APPLICANT: Hu, Shi-Xue
APPLICANT: Benedict, William F
TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and

OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: January 16, 2003, 23.41.58 , Search time 250,854 seconds
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Perfect score: 4017
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Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Post-processing: Minimum Match n%
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 22:   /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
 23:   /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
 24:   /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	% Length	DB	ID	Description
1	4017	100.0	11	23	AAQ04713	Cancer supressing...
2	4017	100.0	11	23	AAQ04713	Retinoblastoma gen
3	4017	100.0	14	19	AAV41544	Retinoblastoma gen
4	4017	100.0	19	21	AAV40004	R-retinoblastoma
5	4017	100.0	21	20	AAX42087	Wild type human re
6	4017	100.0	20	21	AAX90350	Human plu-RB ret.
7	4017	100.0	22	20	AAX00737	cDNA encoding a re
8	4017	100.0	22	22	AAK25755	Retinoblastoma tum
9	4017	100.0	22	23	AAD04474	Retinoblastoma tum
10	4017	100.0	23	23	ABL50904	Cancer supressing
11	4017	100.0	19	15	AAV58445	Modified retinobla
12	4017	100.0	15	19	AAV54991	DNA sequence of th
13	4017	100.0	15	21	AAQ72690	Retinoblastoma 94x
14	4017	100.0	19	19	AAV58444	Modified retinobla
15	4017	100.0	19	19	AAV58443	Modified retinobla
16	4017	100.0	19	19	AAV58446	Modified retinobla
17	4017	100.0	19	19	AAV58442	Modified retinobla
18	4017	100.0	19	19	AAV58441	Modified retinobla
19	4017	100.0	19	19	AAV58447	Modified retinobla
20	4017	100.0	19	19	AAV58452	Modified retinobla
21	4017	100.0	19	19	AAV58440	Modified retinobla
22	4017	100.0	21	19	AAV54990	DNA sequence of th
23	4017	100.0	21	19	AAA25991	Human retinoblasto
24	4017	100.0	24	21	AAZ88444	Human retinoblasto
25	4014	99.9	9	24	AHL62873	Human androgen rec
26	4013	99.9	16	9	AAN81369	Breast cancer rela
27	4013	99.9	16	15	AAQ90059	Human retinoblasto
28	4013	99.9	15	16	AAX70536	Retinoblastoma tum
29	4011	99.9	24	24	ABK84079	Human retinoblasto
30	4010	99.9	20	24	AAQ04501	Human retinoblasto
31	4002	99.7	16	20	AAQ66398	Human RB110 cDNA.
32	3903	97.2	10	16	AAN90489	Human RB110 cDNA.
33	3875	96.5	9	10	AAN81261	CDNA of human reti
34	3674	91.5	19	9	AAV58449	Probe for retinobl
35	3667	91.3	19	19	AAV58451	Modified retinobla
36	3550	88.4	19	19	AAV58450	Modified retinobla
37	3161	78.7	20	19	AAV58448	Modified retinobla
38	1761.5	43.9	10	20	AAX04502	Human retinoblasto
39	1685.5	42.0	10	20	AAN90490	Human retinoblasto
40	772	19.2	24	24	ABK83840	DNA of human retin
41	771	19.2	13	24	AAS94981	Human cDNA differe
42	756	18.8	13	13	AAO32665	Human DNA sequence
43	729.5	18.2	24	24	AAQ84800	Nearly complete pr
44	728.5	18.1	16	23	AAQ82748	Human cDNA differe
45	695.5	15.1	23	23	AAS81193	rb2 retinoblastom

RESULT 1
AAQ04713

ID   AAQ04713 standard; cDNA, 2994 BP.
XX
AC   AAQ04713;
XX
DT   11-OCT-1990 (first entry)
XX
DE   Cancer supressing gene (CSG).
XX
KW   Cancer; cancer supressing gene; CSG; 13q14; retinoblastoma;
KW   ds.
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FH
FT   CDS   139..2922
FT   /*tag= a

ALIGNMENTS

XX
PN   WO9005180-A.
XX
PD   17-MAY-1990.
XX
PF   30-OCT-1989; 89WO-0004808.
XX
PR   31-OCT-1988; 88US-0265829.
XX
PA   (REGC) UNIV OF CAIPORNIA.
XX
PI   Lee WH, Huang HJS;
XX
DR   WPI; 1990-178822/23.
DR   P-PSDB; AAR05305.
XX
PS   Claim 55; Page 86, 105pp; English.
XX
CC   Gene is taken from human chromosome 13q14 retinoblastoma (RB) cDNA.
CC   By installing a working CSG, safe and specific treatment and
CC   prophylaxis can be given to cancer patients.
XX
PT   Controlling cancer
PT   by replacing ineffective cancer suppressing gene with cloned.
PT   active gene.
XX
SQ   Sequence 2994 BP; 974 A; 618 C; 593 G; 809 T; 0 other;

Alignment scores:
Pred. No.:

			Length:	2994
Score:	0	4017.00	Matches:	781
Percent Similarity:	100.00%		Conservative:	0
Percent Identity:	100.00%		Mismatches:	0
Best Local Similarity:	100.00%		Indels:	0
Query Match:	11		Gaps:	0
DB:				

US-09-026-459A-37 (1-781) x AAQ04713 (1-2994)

Qy   1 MetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArg   20
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Db   580 ATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGG   639

Qy   21 ThrCysGluLeuTyrLeuThrGlnProSerSerSerLeuSerThrGlnIleAsnSer   40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   640 ACATGTGAACTATATATTTGACACAACCCAGTGTCGTATAACTACTGAAATAAATTCT   699

Qy   41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln   60
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Db   700 GCATTCGTCCTGTCTAAAAGTTTCTTCGCATCACATTGTTATTAGCCTAAAGGGGAACTA   759

Qy   61 MetGluAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle   80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   760 ATGGAAGATGATCTGGTCATTTCAATTCAGTTAATGCTATGTGTTCTGGACTATTTATT   819

Qy   81 LysLeuSerProMetLeuLysGluProThrTyrTyrThrAlaValIleProIleAsn   100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   820 AAACTCACTCCAATGTTGAAAGAACCAACCTATTATACTGCAGTTATACCAATTAAT   879

Qy   101 GlySerProArgThrProArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu   120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   880 GGTTCACCTCGAACACCAAGGGGGTCAGAACAGGAGTCAGCAAGAATCGCAAAACAACTA   939

Qy   121 GluAspAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu   140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   940 GAAAATGATGACAGAATTATTGAAGTCTGTAAAGAACATGAATGTAATATAGATGAG   999

Qy   141 ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr   160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1000 GTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAACA   1059

Qy   161 SerAsnGlyLeuProGluValGluAspLeuSerLysArgTyrGluGluIleTyrLeuLys   180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1060 TCTAATGGACTTCCAGAGGTTGAAGATCTTTCAAAACGATACGAAGAAATTTATCTTAAA   1119

Qy   181 AsnLysAspAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAsp   200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1120 AATAAAGATGACTTAGATGCAAGGCTGTTCTTGGATCATGATAAAACTCTCCAGACTGAT   1179

Qy   201 IleAspSerPheLysGluGlnLeuLeuArgSerThrSerAspAsnAsnAspGluValAsn   220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1180 ATAGACAGTTTCAAAGAACAGCTACTAAGATCAACAAGTGACAACAATGATGAAGTAAAT   1239

Qy   221 ValLleProTrpHisLeuThrProValAlaArgThrValAlaMetLeuAsnThrIleGln   240
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Db   1240 GTAATTCCCTGGCACCTAACACCAGTAGCAAGAACAGTTGCTATGCTAAACACAATCCAG   1299

Qy   241 IleLeuAsnSerAlaSerAspAspGlnProSerGlnIleSerTyrProGluAsnAsnGly   260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1300 ATTTTAAATTCAGCAAGTGATGATCAACCTTCACAGATTTCATACCCTGAAAATAATGGC   1359

Qy   261 ThrValAspGlyLysGluGluLeuAlaValGlyGlyArgLeuLysLeuGluGluLysLys   280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1360 ACAGTGGAATGCAAAACAACTACTGAAAGGCTTGCAGTTGGAGGACGGTTGAAACTTGAA   1419

Qy   281 GluValSerAlaValValMetGlyArgLeuLysSerIleValSerHisAspLysLysArg   300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1420 GAGAAAAAGGAAGTTTCTGCAAAAGTTGTGGGACAGGGTTGTCAAAGTGTCTCATGACAA   1479

Qy   301 SerIleGlyAsnValIleMetGluSerMetLeuLysSerLeuLeuAsnAspTyrArg   320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1480 TCTATTGGTAATGTTATAATGGAATCCATGTTAAAATCGCTCCTAAATGATTATAGA   1539

Qy   321 LeuLleSerGlnAsnPheSerThrIleProLeuAsnValAsnLeuLysSerAlaArgAsp   340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1540 TTATTCAGTCAAAATTTCAGTACTATTCCTTTAAATGTTAATTTAAAAAGTGCTAGAGAT   1599

Qy   341 AlaCysSerAlaLeuGluValValMetAlaThrTyrSerArgSerIleSerLeuAsnAsp   360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1600 GCGTGCTCCGCTCTTGAGGTTGTAATGGCAACATATTCAAGGAGTATTTCATTAAATGAT   1659

Qy   361 SerGlyThrAspProGlnTyrThrArgProLeuAsnValAsnLeuLysSerValAlaArg   380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1660 TCTGGAACAGATCCACAGTATACTCGGCCCTTAAATGTTAATTTAAAAAGTGTTGCAAGG   1719

Qy   381 PheTyrTrpLysLysValIleGluSerIlePheAlaSerAlaLeuAlaAsn   400
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1720 TTTTACTGGAAGAAAGTGATAGAAAGCATTTTTGCCTCAGCATTGGCTAAT   1779

Qy   401 LysHisGluLeuArgCysGluGlnHisLeuAlaIleMetGluSerLeuAlaTrpPheSer   420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1780 AAACATGAACTACGATGTGAACAACATCTAGCAATCATGGAATCTCTAGCTTGGTTTTCA   1839

Qy   421 ProLeuPheAspLeuLleLysGlyAspLeuGluAspLysAlaHisProGlnHis   440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1840 CCTTTATTTGATCTTATTAAAGGAGACTTGGAAGATAAAGCACATCCTCAGCATTCA   1899

Qy   441 SerAlaCysProLeuGluProLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeu   460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1900 TCTGCATGTCCTCTGGAACCCTTGCAGAATAATCATACTGCTGCAGATATGTATCTTGAA   1959

Qy   461 SerProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsn   480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1960 TCTCCAGTTAGGTCTCCTAAAAAGAAAGGATCAACTACTCGTGTTAATTCAACTGCTAAT   2019

Qy   481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLysProLeuLysSerThrSerLeu   500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2020 GCAGAGACTCAAGCTACTTCAGCATTTCAGACACAGAAGCCACTGAAATCTACTTCTCTG   2079

Qy   501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGlu   520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2080 TCACTGTTTTATAAAAAAGTGTATCGGCTAGCGTATCTCCGGCTAAATACACTTTGTGAA   2139

Qy   521 ArgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPheGlnHisThr   540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2140 CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACTCTGTTCCAGCACACC   2199

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Qy   541 LeuGlnAsnGluTyrGluLeuMetArgGlnHisLeuAspGlnIleMetMetCysSer 560
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2200 CTCCAGAATGAGTATGAGCTCATGAGACAGCATTTGGACCAAAATTATGATGTGTTCC 2259

Qy   561 MetTyrGlyIleCysLysValLysAsnIleAspLeuLysPhePheLysIleIleValThrAla 580
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2260 ATGTATGGCCATATGCAAAGTGAAGAAATATAGACCTTAAATTCAAAATCATTGTAACACGA 2319

Qy   581 TyrGlyAspLeuProHisAlaValAlaValGlnThrPheLysArgValLeuIleLysGluGlu 600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2320 TACAAGGACCTTCCTCATGCCGTTGCAGTGCAGACATTCAAACGTGTTTTGATCAAGGAGAG 2379

Qy   601 GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsn 620
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2380 GAGTATGATTCTATTATTGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAAT 2439

Qy   621 IleLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHisIleProArg 640
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2440 ATTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCGA 2499

Qy   641 SerProTyrLysPheProSerSerProLeuArgIleProGlyGlyAsnIleTyrIleSer 660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2500 AGCCCTTACAAGTTTCCTTCGTCACCCTTACGCATTCCTGGAGGAAATATCTATATTTCA 2559

Qy   661 ProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrPro 680
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2560 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAAAAATGACTCCA 2619

Qy   681 ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGluLysPheGlnLys 700
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2620 AGATCAAGAATCTTAGTATCAAATTGGTGAAAGCTTCGGGACTTCTGAGAAGTTCCAGAAA 2679

Qy   701 IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsn 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2680 ATAAATCAGATGGTATGTAACAGCGACCGTGTTCTCAAAAGAAGTGCTGAAGGAAGCAAC 2739

Qy   721 ProProLysProLeuLysLysLeuArgPheAspIleGluGlyTyrAspGluAlaAspGly 740
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2740 CCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGGATACGATGAAGCAGATGGA 2799

Qy   741 SerLysHisLeuProGlyGluSerProPheGlnIleGlyLeuAlaGluMetThrSerThr 760
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2800 AGTAAACACTTCCCAGGAGAGTCCCAATTTCAGAAAGGCAGAAATGACTTCTACT 2859

Qy   761 ArgThrArgMetGlnLysGlnLysMetAsnAspThrSerAsnLysGluGlu 780
         |||||||||||||||||||||||||||||||||||||||||||
Db  2860 CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCACTAACAAGGAAGAG 2919

Qy   781 Lys 781
         |||
Db  2920 AAA 2922
```

```
RESULT 2
AAQ41545
ID   AAQ41545 standard, DNA, 2994 BP.
XX
AC   AAQ41545;
XX
DT   24-AUG-1993  (first entry)
XX
DE   Retinoblastoma gene.
XX
KW   RB gene product; p56RB portion; cell cycle progression control;
KW   combination; therapeutic methods; arrest; tumourigenesis;
KW   regulation; physiological processes; blood cell prodn.; ss.
KW   gamete prodn.; ss.
XX
OS   Homo sapiens SR-40 cell line.
XX
FH   Key             Location/Qualifiers
FT   CDS             139..2925
FT                   /*tag= a
FT                   /note= "Rb protein"
```

Method of controlling cell cycle progression - uses purified retinoblastoma protein or fragment, for use in combination with therapeutic methods to arrest tumorigenesis

Disclosure; Fig 9; 68pp; English.

```
CC   The sequence is that of the retinoblastoma gene which encodes the
CC   retinoblastoma (RB) protein which may be used as part of a method of
CC   controlling cell cycle progression which may be used in combination
CC   with therapeutic methods to arrest tumorigenesis in organisms. The
CC   cell cycle can be reversibly arrested in a convenient and safe
CC   manner. The protein is used in a compsn. is relatively inexpensive
CC   and readily obtainable, and shows little or no toxic effects on
CC   healthy cells. It is also compatible with other methods and devices
CC   for regulating certain physiological processes of the body, such as
CC   blood cell prodn. and gamete prodn. Fragments of the protein are
CC   soluble in low concns. of glycerol thus enhancing their value in
CC   pharmaceutical applicns.
XX
SQ   Sequence 2994 BP; 974 A; 618 C; 594 G; 808 T; 0 other;
```

```
Alignment Scores:
Pred. No.:
Score:                     0          Length:        2994
Pred. No.:               401/00       Matches:       781
Percent Similarity:     100.00%       Conservative:  0
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            100.00%       Indels:        0
DB:                     14            Gaps:          0
```

us-09-026-459A-37 (1-781) x AAQ41545 (1-2994)

```
Qy     1 MetSerArgProLeuLeuLysLysLysTyrAspValLeuPheAlaLeuPheSerLysGluArg 20
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   580 ATGTCAAGACCTGTTGAAGAAGTATGATGTTATTTGCACTCTTCAGCCAAAATTGGAAAGG 639

Qy    21 ThrCysSerGluGlnIleThrTyrLeuThrGlnProSerSerIleSerThrGluIleAsnSer 40
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   640 ACAATGTAGAACTTATATTATTTGCACACACCCCAGCACTTCGAGATCTACTGAAATAAATTCT 699

Qy    41 AlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGln 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   700 GCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAGGGGAAGTATTACAA 759

Qy    61 MetGluAspSerAspLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle 80
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   760 ATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATT 819

Qy    81 LysLeuSerProMetLeuLysGluHisGlyAsnAsnArgSerAlaArgIleAlaLysGluAsn 100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   820 AAACTCAGTCCAATGTTGCTCAAAGAACCATATAAAACAGCATCCATTTAAT 879

Qy   101 GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGluLeu 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   880 GGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACACTA 939

Qy   121 GluAsnAspThrArgIleIleGlyValLeuCysLysGluHisGlyAsnIleAspGlu 140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

GenCore version 5.1.3

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OM protein - nucleic search, using frame-plus-p2n model

Run on: January 18, 2003, 04.12.19 , Search time 44.4279 seconds
                                            (without alignments)
                                            5391.080 Million cell updates/sec

Title: US-09-026-459A-37
Perfect score: 4017
Sequence: 1 MSRLLKKYDVLFALFSKLER   TPMLKLKMNDSMPTSNKEEK 78!

Scoring table: BLOSUM62
               Xgapext   0.5
               Ygapop 10.0   Xgapext   0.5
               Ygapop 10.0   Ygapext   0.5
               Fgapop   6.0   Fgapext   7.0
               Delop   6.0   Delext   7.0
               Delop   6.0   Delext   7.0

Searched: 41362 seqs, 15338381 residues   #82744

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-YGAPOP=10 -YGAPEXT-0.5 -DELOP-6 -DELEXT=7

Database :

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   2: /cgn2_6/ptodata/1/ina/5B_COMB seq:*
   3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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   5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
   6: /cgn2_6/ptodata/1/ina/backfiles] seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	4017	100.0	2994	1	US-08-204-329-2	Sequence 2, Appli
2	4017	100.0	2994	2	US-08-482-527 4	Sequence 4, Appli
3	4017	100.0	2994	3	US-08-801-092-3	Sequence 3, Appli
4	4017	100.0	2994	4	US-09-315-113-3	Sequence 3, Appli
5	4017	100.0	2995	2	US-08-959-638-7	Sequence 7, Appli
6	4017	100.0	3232	2	US-08-038-760-7	Sequence 3, Appli
7	4017	100.0	3212	1	US-08-038-760-1	Sequence 7, Appli
8	4017	100.0	3232	2	US-08-038-760-2	Sequence 2, Appli
9 c	4017	100.0	3232	2	US-08-470-091-1	Sequence 2, Appli
10 c	4014	100.0	3232	2	US-08-470-091-2	Sequence 1, Appli
11	4007	99.8	2994	5	PCT-US94-10357-1	Sequence 1, Appli
12	768	19.1	2808	1	US-07-708-962-1	Sequence 1, Appli

RESULT 1
us-08-204-329-2

Sequence 2 , Application US/08204329
Patent No. 5712255

GENERAL INFORMATION:
  APPLICANT:
  APPLICANT: SHEPARD, H. M.
  APPLICANT: WEN, SHU F.
  TITLE OF INVENTION: CHARACTERIZATION OF A NOVEL ANTI-P110RB
  TITLE OF INVENTION: MONOCLONAL ANTIBODY
  NUMBER OF SEQUENCES: 2
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
    STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
    CITY: SAN FRANCISCO
    STATE: CALIFORNIA
    COUNTRY: U.S.A.
    ZIP: 94111
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/204,329
    FILING DATE: 15-AUG-1994
    CLASSIFICATION: 435
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: PCT/US92/05866
    FILING DATE: 14-JUL-1992
  ATTORNEY/AGENT INFORMATION:
    NAME: RENEE A PITTS
    REGISTRATION NUMBER: 35,136
    REFERENCE/DOCKET NUMBER: 16930-0004000US
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (415) 326-2400
    TELEFAX: (415) 326-2422

ALIGNMENTS

(Columns: residue position, score value, DB ID, Sequence/Application)

13	19.0	2808	US-09-152-721b-1	Sequence 2, Appli
14	729.5	18.2	4853	US-08-832-883-1	Sequence 1, Appli
15	729.5	18.2	4853	US-08-832 877	Sequence 1, Appli
16	727.5	18.1	3249	US-08-106-493A-1	Sequence 1, Appli
17	727.5	18.1	3249	US-08-129-264-1	Sequence 1, Appli
18	516.5	12.9	3747	US-09-211-293B-2	Sequence 2, Appli
19	144	3.6	6773	US-09-166-350-27	Sequence 27, Appli
20	143.5	3.6	3763	US-07-792-865D-1	Sequence 1, Appli
21	143	3.6	3593	US-09-404-627-3	Sequence 3, Appli
22	143	3.6	4205	US-09-404-627-1	Sequence 1, Appli
23	140	3.5	4789	US-08-328-254 5	Sequence 5, Appli
24	138	3.4	3883	US-09-723-820-3	Sequence 3, Appli
25	138	3.4	3883	US-09-468-036-33	Sequence 33, Appli
26	138	3.4	3884	US-09-376-943-23	Sequence 27, Appli
27	138	3.4	3884	US-09-541-780-3	Sequence 3, Appli
28	138	3.4	4868	US-08-939-937-12	Sequence 12, Appli
29	137	3.4	4595	US-09-541-780-12	Sequence 12, Appli
30	137	3.4	10135	US-09-451-769-2	Sequence 2, Appli
31	137	3.4	10146	PCT-US95-16216-2	Sequence 2, Appli
32	131	3.3	2415	US-09-134-001C-2381	Sequence 2381, Ap
33	131	3.3	2415	US-09-752-188-44	Sequence 54, Appli
34	130	3.2	5893	US-08-687-080 44	Sequence 44, Appli
35	130	3.2	5181	US-08-961-527-29	Sequence 19, Appli
36	127.5	3.2	5254	US-08-961-527-29	Sequence 29, Appli
37	121	3.0	5361	US-08-973-462-2	Sequence 2, Appli
38	121	3.0	6152	US-08-973-462-1	Sequence 1, Appli
39	119	3.0	40544	US-09-134-001C-322	Sequence 322, App
40	118.5	2.9	40544	US-08-923-992A-9	Sequence 9, Appli
41	117.5	2.9	3492	US-08-212-133A-7	Sequence 7, Appli
42	117.5	2.9	7493	US-08-474-503-5	Sequence 5, Appli
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INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 2994 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: DNA (cDNA)

US-08-204-329 2

Alignment Scores:
Pred. No.:

		length:	2994
Score:	4017.00	Matches:	781
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
		Gaps:	0

US-09-026-459-37 (2994) x US-08-204-329 2 (1-2994)

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Db  2500  AGCCCTTACAAGTTCCTAGTTCACCCTTACGGATTCCTGGAGGCGAACATCTATATTTCA   2559

Qy   661  ProLeuLysSerProTyrLysIleSerGlyGlyLeuProThrProThrLysMetThrPro   680
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Db  2560  CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAAACAAAATGACTCCA        2619

Qy   681  ArgSerArgIleLeuValSerLeuGlyGluSerPheGlyThrSerGluLysPheGlnLys   700
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Db  2620  AGATCAAGAATTTTATAT-AATC-GTAA-CATT-GG-A-TT-TA-AATT-T-A-AA       2679

Qy   701  IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsn   720
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Db  2680  ATAAATCAGATGGTATGTAACAGCGACCGTGTCTCAAAAGAAGTGCTGAAGCAAGCAAC   2739

Qy   721  ProProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGly   740
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Qy   741  SerLysHisLeuProGlyGluSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr   760
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Qy   781  Lys   781
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Db  2920  AAA   2922
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RESULT 2
US-08-482-627-4
Sequence 4, Application US/08482627
Patent No. 5598134
GENERAL INFORMATION:
  APPLICANT: Lee, Wen-Hwa
  APPLICANT: Lee, Eva Y-H.P
  TITLE OF INVENTION: Retinoblastoma Gene - Cancer Suppressor
  TITLE OF INVENTION: and Regulator
  NUMBER OF SEQUENCES: 5
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Campbell and Flores
    STREET: 4370 La Jolla Village Drive, Suite 700
    CITY: San Diego
    STATE: California
    COUNTRY: United States
    ZIP: 92122
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/482,627
    FILING DATE: 07-JUN-1995
    CLASSIFICATION: 435
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 07/951,947
    FILING DATE: 28-SEP-1992
  ATTORNEY/AGENT INFORMATION:
    NAME: Campbell, Cathryn A.
    REGISTRATION NUMBER: 31,815
    REFERENCE/DOCKET NUMBER: P-nc 1707
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (619) 535-9001
    TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4
  SEQUENCE CHARACTERISTICS:
    LENGTH: 2994 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  FEATURE:
    NAME/KEY: CDS
    LOCATION: 139..2924

US-08-482-627-4

Alignment Scores:

Pred. No.:	0
Score:	4017.00
Percent Similarity:	100.00%
Percent Identity:	100.00%
Query Match:	100.00%
DB:	

Length:	2994
Matches:	781
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-026-459a-37 (1-781) x US-08-482-627-4 (1-2994)

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Qy    21  ThrCysGluLeuGlyThrLeuThrGluLeuThrSerSerLeuSerSerGluThrGluSer    40
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Qy    41  AlaLeuValLeuLysValSerTrpIleThrPhePheLeuLeuAlaLysGlyValLeuGln    60
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Qy    61  MetGluAspAspSerLeuValIleSerPheGlnLeuMetLeuCysValLeuAspTyrPheIle    80
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Qy    81  LysLeuSerProProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn   100
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Qy   101  GlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeu   120
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Qy   121  GluAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsnIleAspGlu   140
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Qy   141  ValLysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThr   160
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Qy   161  SerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGluGluIleTyrLeuLys   180
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Qy   201  IleAsnSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGluGluVal    220
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Db  1180  ATAAATAGTTTTGAAACACAGAGAACACCTAGAAAGTCAAATCTAGATGAAGAAGTA    1239

Qy   221  ValLeuProProGlnHisProIleArgThrValMetAsnThrIleGlnGlnLeuMet    240
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Db  1240  GTAACTCCACAACATCCAATTAGGACAGTTATGAACACAATTCAACAACTCATG       1299

Qy   241  IleLeuAsnAsnGluLysAspAlaSerArgSerAspLeuLysAsnTyrIleLysLys    260
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Db  1300  ATTTTAAATAATGAAAAAGATGCATCTAGATCTGATTTAAAGAACTATATAAAGAAA    1359

Qy   261  IleValAsnProGlyGlnSerIleGlnLeuLysArgValLysAspIleGlyTyrIleLys    280
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